

SEQUENCE LISTING

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Merkins, Louise
Bennett, Robert
Seiss, Donald

<120> Mammalian DNA Binding Membrane-Associated Protein-encoding Gene and Uses

<130> 00-617-A

<140> US 09/921,099

<141> 2001-08-01

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cca atg caa agg aaa ctg gtg aca ctt gta aac tgt caa ctg gtg gag	1033
Pro Met Gln Arg Lys Leu Val Thr Leu Val Asn Cys Gln Leu Val Glu	
130 135 140	
gaa gaa ggt cgt gta aga gcc atg cga gca gct cgt tcc ctt gga gaa	1081
Glu Glu Gly Arg Val Arg Ala Met Arg Ala Ala Arg Ser Leu Gly Glu	
145 150 155 160	
aga act gta aca gaa ctg ata tta cag cac cag aac cct cag cag ttg	1129

Arg	Thr	Val	Thr	Glu	Leu	Ile	Leu	Gln	His	Gln	Asn	Pro	Gln	Gln	Leu	
				165				170						175		
tct	gcc	aat	cta	tgg	gcc	gct	gtc	agg	gct	cga	gga	tgc	cag	ttt	tta	1177
Ser	Ala	Asn	Leu	Trp	Ala	Ala	Val	Arg	Ala	Arg	Gly	Cys	Gln	Phe	Leu	
			180					185					190			
ggg	cca	gct	atg	caa	gaa	gag	gcc	ttg	aag	ctg	gtg	tta	ctg	gca	tta	1225
Gly	Pro	Ala	Met	Gln	Glu	Glu	Ala	Leu	Lys	Leu	Val	Leu	Leu	Ala	Leu	
			195				200					205				
gaa	gat	ggg	tct	gcc	ctc	tca	agg	aaa	gtt	ctg	gta	ctt	ttt	gtt	gtg	1273
Glu	Asp	Gly	Ser	Ala	Leu	Ser	Arg	Lys	Val	Leu	Val	Leu	Phe	Val	Val	
	210					215					220					
cag	aga	cta	gaa	cca	aga	ttt	cct	cag	gca	tca	aaa	aca	agt	att	ggg	1321
Gln	Arg	Leu	Glu	Pro	Arg	Phe	Pro	Gln	Ala	Ser	Lys	Thr	Ser	Ile	Gly	
225					230				235						240	
cat	gtt	gtg	caa	cta	ctg	tat	cga	gct	tct	tgt	ttt	aag	gtt	acc	aaa	1369
His	Val	Val	Gln	Leu	Leu	Tyr	Arg	Ala	Ser	Cys	Phe	Lys	Val	Thr	Lys	
			245					250						255		
aga	gat	gaa	gac	tct	tcc	cta	atg	cag	ctg	aag	gag	gaa	ttt	cgg	agt	1417
Arg	Asp	Glu	Asp	Ser	Ser	Leu	Met	Gln	Leu	Lys	Glu	Glu	Phe	Arg	Ser	
			260					265					270			
tat	gaa	gca	tta	cgc	aga	gaa	cat	gat	gcc	caa	att	gtt	cat	att	gcc	1465
Tyr	Glu	Ala	Leu	Arg	Arg	Glu	His	Asp	Ala	Gln	Ile	Val	His	Ile	Ala	
	275						280					285				
atg	gaa	gca	gga	ctc	cgt	att	tca	cct	gaa	cag	tgg	tcc	tct	ctt	ttg	1513
Met	Glu	Ala	Gly	Leu	Arg	Ile	Ser	Pro	Glu	Gln	Trp	Ser	Ser	Leu	Leu	
	290					295					300					
tat	ggg	gat	ttg	gct	cat	aaa	tca	cac	atg	cag	tct	atc	att	gat	aag	1561
Tyr	Gly	Asp	Leu	Ala	His	Lys	Ser	His	Met	Gln	Ser	Ile	Ile	Asp	Lys	
305					310				315						320	
cta	cag	tct	cca	gag	tca	ttt	gca	aag	agt	gtc	cag	gaa	ttg	aca	att	1609
Leu	Gln	Ser	Pro	Glu	Ser	Phe	Ala	Lys	Ser	Val	Gln	Glu	Leu	Thr	Ile	
				325					330					335		
gtt	ttg	caa	cga	aca	ggg	gac	cca	gct	aac	tta	aat	aga	ctg	agg	cct	1657
Val	Leu	Gln	Arg	Thr	Gly	Asp	Pro	Ala	Asn	Leu	Asn	Arg	Leu	Arg	Pro	
			340					345					350			
cat	tta	gag	ctt	ctt	gca	aac	ata	gac	cct	aat	cca	gac	gct	gtt	tca	1705
His	Leu	Glu	Leu	Leu	Ala	Asn	Ile	Asp	Pro	Asn	Pro	Asp	Ala	Val	Ser	
			355				360					365				
cca	act	tgg	gag	cag	ctg	gaa	aat	gca	atg	gta	gct	gtt	aaa	aca	gta	1753
Pro	Thr	Trp	Glu	Gln	Leu	Glu	Asn	Ala	Met	Val	Ala	Val	Lys	Thr	Val	
	370					375					380					
gtt	cat	ggc	ctt	gtg	gac	ttc	ata	caa	aat	tat	agt	aga	aaa	ggc	cat	1801
Val	His	Gly	Leu	Val	Asp	Phe	Ile	Gln	Asn	Tyr	Ser	Arg	Lys	Gly	His	

385	390	395	400	
gag acc cct cag cct cag cca aac agc aaa tac aag act agc atg tgc				1849
Glu Thr Pro Gln Pro Gln Pro Asn Ser Lys Tyr Lys Thr Ser Met Cys	405	410	415	
cga gat ttg cga cag cag ggg ggt tgt cca cga gga aca aat tgt aca				1897
Arg Asp Leu Arg Gln Gln Gly Gly Cys Pro Arg Gly Thr Asn Cys Thr	420	425	430	
ttt gcc cat tct cag gaa gag ctt gaa aag tat cga tta agg aac aaa				1945
Phe Ala His Ser Gln Glu Glu Leu Glu Lys Tyr Arg Leu Arg Asn Lys	435	440	445	
aag atc aat gcc act gta aga acg ttt cct ctt cta aat aaa gtt ggt				1993
Lys Ile Asn Ala Thr Val Arg Thr Phe Pro Leu Leu Asn Lys Val Gly	450	455	460	
gta aac aac act gtc aca acc aca gcc gga aat gtc att tct gtc ata				2041
Val Asn Asn Thr Val Thr Thr Thr Ala Gly Asn Val Ile Ser Val Ile	465	470	475	480
gga agt act gaa aca aca ggg aaa att gtt cca agt aca aac gga att				2089
Gly Ser Thr Glu Thr Thr Gly Lys Ile Val Pro Ser Thr Asn Gly Ile	485	490	495	
tca aat gca gaa aac agt gtt tcc cag cta atc tca cgt agt act gac				2137
Ser Asn Ala Glu Asn Ser Val Ser Gln Leu Ile Ser Arg Ser Thr Asp	500	505	510	
agt acc tta aga gct ctg gag acc gtg aag aaa gtg gga aag gtt ggc				2185
Ser Thr Leu Arg Ala Leu Glu Thr Val Lys Lys Val Gly Lys Val Gly	515	520	525	
gct aat ggt cag aat gct gct ggg ccc tct gca gat tct gta act gaa				2233
Ala Asn Gly Gln Asn Ala Ala Gly Pro Ser Ala Asp Ser Val Thr Glu	530	535	540	
aat aaa att ggt tct cca ccc aag act cct gta agt aat gta gca gct				2281
Asn Lys Ile Gly Ser Pro Pro Lys Thr Pro Val Ser Asn Val Ala Ala	545	550	555	560
acc tca gct ggg ccc tct aat gtt gga aca gag ctg aat tct gtg cct				2329
Thr Ser Ala Gly Pro Ser Asn Val Gly Thr Glu Leu Asn Ser Val Pro	565	570	575	
caa aaa tcc agc cca ttt cta act aga gta cca gta tat cct ccg cat				2377
Gln Lys Ser Ser Pro Phe Leu Thr Arg Val Pro Val Tyr Pro Pro His	580	585	590	
tct gaa aac att cag tat ttt caa gat cca agg act cag ata ccc ttt				2425
Ser Glu Asn Ile Gln Tyr Phe Gln Asp Pro Arg Thr Gln Ile Pro Phe	595	600	605	
gaa gtc cca cag tac cca cag aca gga tac tat cca cca cct cca acg				2473
Glu Val Pro Gln Tyr Pro Gln Thr Gly Tyr Tyr Pro Pro Pro Pro Thr	610	615	620	

gta cca gct ggt gtg gct ccc tgt gtt cct cgc ttt gtg agg tcc aat Val Pro Ala Gly Val Ala Pro Cys Val Pro Arg Phe Val Arg Ser Asn 625 630 635 640	2521
aac gtt cca gag tcc tcc ctc cca cct gct tcc atg cca tat gcc gat Asn Val Pro Glu Ser Ser Leu Pro Pro Ala Ser Met Pro Tyr Ala Asp 645 650 655	2569
cat tac agt aca ttt tcc cct cga gat cga atg aat tct tct cct tac His Tyr Ser Thr Phe Ser Pro Arg Asp Arg Met Asn Ser Ser Pro Tyr 660 665 670	2617
cag cct cct cct ccg cag ccg tat gga cca gtt cct cca gta cct tct Gln Pro Pro Pro Gln Pro Tyr Gly Pro Val Pro Pro Val Pro Ser 675 680 685	2665
gga atg tat gct cct gtg tac gac agc agg cgc atc tgg cgc cca cct Gly Met Tyr Ala Pro Val Tyr Asp Ser Arg Arg Ile Trp Arg Pro Pro 690 695 700	2713
atg tac caa cga gat gac att att aga agc aat tct tta cct cca atg Met Tyr Gln Arg Asp Asp Ile Ile Arg Ser Asn Ser Leu Pro Pro Met 705 710 715 720	2761
gat gtg atg cac tca tct gtc tat cag aca tct ttg cgg gaa aga tat Asp Val Met His Ser Ser Val Tyr Gln Thr Ser Leu Arg Glu Arg Tyr 725 730 735	2809
aac tca tta gat gga tat tat tcg gtg gct tgt cag cca cca agt gag Asn Ser Leu Asp Gly Tyr Tyr Ser Val Ala Cys Gln Pro Pro Ser Glu 740 745 750	2857
cca agg aca act gtg cct tta cca agg gaa cct tgt ggt cat ttg aag Pro Arg Thr Val Pro Leu Pro Arg Glu Pro Cys Gly His Leu Lys 755 760 765	2905
acc agt tgc gag gag cag ata aga aga aag cca gat cag tgg gca cag Thr Ser Cys Glu Glu Gln Ile Arg Arg Lys Pro Asp Gln Trp Ala Gln 770 775 780	2953
tac cac act cag aaa gca cct ctt gtc tct tca act ctt cct gtg gca Tyr His Thr Gln Lys Ala Pro Leu Val Ser Ser Thr Leu Pro Val Ala 785 790 795 800	3001
aca cag tca cca aca cca cct tct cct ctg ttc agt gta gac ttt cgt Thr Gln Ser Pro Thr Pro Pro Ser Pro Leu Phe Ser Val Asp Phe Arg 805 810 815	3049
gcg gat ttc tca gag agt gtg agt ggt aca aaa ttt gaa gaa gat cat Ala Asp Phe Ser Glu Ser Val Ser Gly Thr Lys Phe Glu Glu Asp His 820 825 830	3097
ctt tcc cat tat tct ccc tgg tct tgt ggc acc ata ggc tcc tgt ata Leu Ser His Tyr Ser Pro Trp Ser Cys Gly Thr Ile Gly Ser Cys Ile 835 840 845	3145

aat gcc att gat tca gag ccc aaa gat gtc att gct aat tca aat gct	3193
Asn Ala Ile Asp Ser Glu Pro Lys Asp Val Ile Ala Asn Ser Asn Ala	
850 855 860	
gtg tta atg gac ctg gac agt ggt gat gtt aag aga aga gta cat tta	3241
Val Leu Met Asp Leu Asp Ser Gly Asp Val Lys Arg Arg Val His Leu	
865 870 875 880	
ttt gaa acc cag aga agg aca aaa gaa gaa gat cca ata att ccc ttt	3289
Phe Glu Thr Gln Arg Arg Thr Lys Glu Glu Asp Pro Ile Ile Pro Phe	
885 890 895	
agt gat gga ccc atc atc tca aaa tgg ggt gcg att tcc aga tct tcc	3337
Ser Asp Gly Pro Ile Ile Ser Lys Trp Gly Ala Ile Ser Arg Ser Ser	
900 905 910	
cgt aca ggt tac cat acc aca gat cct gtc cag gcc act gct tcc caa	3385
Arg Thr Gly Tyr His Thr Thr Asp Pro Val Gln Ala Thr Ala Ser Gln	
915 920 925	
gga agt gcg act aag ccc atc agt gta tca gat tat gtc cct tat gtc	3433
Gly Ser Ala Thr Lys Pro Ile Ser Val Ser Asp Tyr Val Pro Tyr Val	
930 935 940	
aat gct gtt gat tca agg tgg agt tca tat ggc aac gag gcc aca tca	3481
Asn Ala Val Asp Ser Arg Trp Ser Ser Tyr Gly Asn Glu Ala Thr Ser	
945 950 955 960	
tca gca cac tat gtt gaa agg gac aga ttc att gtt act gat tta tct	3529
Ser Ala His Tyr Val Glu Arg Asp Arg Phe Ile Val Thr Asp Leu Ser	
965 970 975	
ggt cat aga aag cat tcc agt act ggg gac ctt ttg agc ctt gaa ctt	3577
Gly His Arg Lys His Ser Ser Thr Gly Asp Leu Leu Ser Leu Glu Leu	
980 985 990	
cag cag gcc aag agc aac tca tta ctt ctt cag aga gag gcc aat gct	3625
Gln Gln Ala Lys Ser Asn Ser Leu Leu Leu Gln Arg Glu Ala Asn Ala	
995 1000 1005	
ttg gcc atg caa cag aag tgg aat tcc ctg gat gaa ggc cgt cac	3670
Leu Ala Met Gln Gln Lys Trp Asn Ser Leu Asp Glu Gly Arg His	
1010 1015 1020	
ctt acc tta aac ctt tta agc aag gaa att gaa cta aga aat gga	3715
Leu Thr Leu Asn Leu Leu Ser Lys Glu Ile Glu Leu Arg Asn Gly	
1025 1030 1035	
gag tta cag agt gat tat aca gaa gat gca aca gat act aaa cct	3760
Glu Leu Gln Ser Asp Tyr Thr Glu Asp Ala Thr Asp Thr Lys Pro	
1040 1045 1050	
gat agg gat atc gag tta gag ctt tca gca ctt gat act gat gaa	3805
Asp Arg Asp Ile Glu Leu Glu Leu Ser Ala Leu Asp Thr Asp Glu	
1055 1060 1065	
cct gat gga caa agt gaa cca att gaa gag atc ttg gac ata cag	3850

Pro Asp Gly Gln Ser Glu Pro Ile Glu Glu Ile Leu Asp Ile Gln 1070 1075 1080	
ctt ggt atc agt tct caa aat gat cag ttg cta aat gga atg gca Leu Gly Ile Ser Ser Gln Asn Asp Gln Leu Leu Asn Gly Met Ala 1085 1090 1095	3895
gtg gaa aat ggg cat cca gta cag cag cac caa aag gag cca cca Val Glu Asn Gly His Pro Val Gln Gln His Gln Lys Glu Pro Pro 1100 1105 1110	3940
aag cag aag aaa cag agt tta ggt gaa gac cat gtg att ctg gag Lys Gln Lys Lys Gln Ser Leu Gly Glu Asp His Val Ile Leu Glu 1115 1120 1125	3985
gag caa aaa aca att ctg ccg gta act tct tgc ttt agc cag cca Glu Gln Lys Thr Ile Leu Pro Val Thr Ser Cys Phe Ser Gln Pro 1130 1135 1140	4030
ctc cca gtg tct att agc aat gca agt tgc ctc ccc atc acc aca Leu Pro Val Ser Ile Ser Asn Ala Ser Cys Leu Pro Ile Thr Thr 1145 1150 1155	4075
tct gtc agt gct ggc aac ctc att ctg aaa act cat gtt atg tct Ser Val Ser Ala Gly Asn Leu Ile Leu Lys Thr His Val Met Ser 1160 1165 1170	4120
gaa gat aaa aac gac ttt tta aaa cct gtt gca aat ggg aag atg Glu Asp Lys Asn Asp Phe Leu Lys Pro Val Ala Asn Gly Lys Met 1175 1180 1185	4165
gtt aac agc tgaaaggagg ttcattctttc aaatttgatga ccacaccatg Val Asn Ser 1190	4214
gaagcattta cactagcttt ttatatatat aatatatatt atataatgta tatttttttt	4274
aaaaaaaaga tattactggg ggcattccatt tcctgtggac tctttgatac ttcaagccct	4334
cttgcattag cattatg	4351

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 <212> PRT
 <213> Homo sapiens

<400> 4

Met Ala Val Gln Ala Ala Gln Trp Thr Glu Phe Leu Ser Cys Pro Ile
1 5 10 15

Cys Tyr Asn Glu Phe Asp Glu Asn Val His Lys Pro Ile Ser Leu Gly
20 25 30

Cys Ser His Thr Val Cys Lys Thr Cys Leu Asn Lys Leu His Arg Lys
 35 40 45

Ala Cys Pro Phe Asp Gln Thr Ala Ile Asn Thr Asp Ile Asp Val Leu
 50 55 60

Pro Val Asn Phe Ala Leu Leu Gln Leu Val Gly Ala Gln Val Pro Asp
 65 70 75 80

His Gln Ser Ile Lys Leu Ser Asn Leu Gly Glu Asn Lys His Tyr Glu
 85 90 95

Val Ala Lys Lys Cys Val Glu Asp Leu Ala Leu Tyr Leu Lys Pro Leu
 100 105 110

Ser Gly Gly Lys Gly Val Ala Ser Leu Asn Gln Ser Ala Leu Ser Arg
 115 120 125

Pro Met Gln Arg Lys Leu Val Thr Leu Val Asn Cys Gln Leu Val Glu
 130 135 140

Glu Glu Gly Arg Val Arg Ala Met Arg Ala Ala Arg Ser Leu Gly Glu
 145 150 155 160

Arg Thr Val Thr Glu Leu Ile Leu Gln His Gln Asn Pro Gln Gln Leu
 165 170 175

Ser Ala Asn Leu Trp Ala Ala Val Arg Ala Arg Gly Cys Gln Phe Leu
 180 185 190

Gly Pro Ala Met Gln Glu Glu Ala Leu Lys Leu Val Leu Leu Ala Leu
 195 200 205

Glu Asp Gly Ser Ala Leu Ser Arg Lys Val Leu Val Leu Phe Val Val
 210 215 220

Gln Arg Leu Glu Pro Arg Phe Pro Gln Ala Ser Lys Thr Ser Ile Gly
 225 230 235 240

His Val Val Gln Leu Leu Tyr Arg Ala Ser Cys Phe Lys Val Thr Lys
 245 250 255

Arg Asp Glu Asp Ser Ser Leu Met Gln Leu Lys Glu Glu Phe Arg Ser

260

265

270

Tyr Glu Ala Leu Arg Arg Glu His Asp Ala Gln Ile Val His Ile Ala
275 280 285

Met Glu Ala Gly Leu Arg Ile Ser Pro Glu Gln Trp Ser Ser Leu Leu
290 295 300

Tyr Gly Asp Leu Ala His Lys Ser His Met Gln Ser Ile Ile Asp Lys
305 310 315 320

Leu Gln Ser Pro Glu Ser Phe Ala Lys Ser Val Gln Glu Leu Thr Ile
325 330 335

Val Leu Gln Arg Thr Gly Asp Pro Ala Asn Leu Asn Arg Leu Arg Pro
340 345 350

His Leu Glu Leu Leu Ala Asn Ile Asp Pro Asn Pro Asp Ala Val Ser
355 360 365

Pro Thr Trp Glu Gln Leu Glu Asn Ala Met Val Ala Val Lys Thr Val
370 375 380

Val His Gly Leu Val Asp Phe Ile Gln Asn Tyr Ser Arg Lys Gly His
385 390 395 400

Glu Thr Pro Gln Pro Gln Pro Asn Ser Lys Tyr Lys Thr Ser Met Cys
405 410 415

Arg Asp Leu Arg Gln Gln Gly Gly Cys Pro Arg Gly Thr Asn Cys Thr
420 425 430

Phe Ala His Ser Gln Glu Glu Leu Glu Lys Tyr Arg Leu Arg Asn Lys
435 440 445

Lys Ile Asn Ala Thr Val Arg Thr Phe Pro Leu Leu Asn Lys Val Gly
450 455 460

Val Asn Asn Thr Val Thr Thr Thr Ala Gly Asn Val Ile Ser Val Ile
465 470 475 480

Gly Ser Thr Glu Thr Thr Gly Lys Ile Val Pro Ser Thr Asn Gly Ile
485 490 495

Ser Asn Ala Glu Asn Ser Val Ser Gln Leu Ile Ser Arg Ser Thr Asp
 500 505 510

Ser Thr Leu Arg Ala Leu Glu Thr Val Lys Lys Val Gly Lys Val Gly
 515 520 525

Ala Asn Gly Gln Asn Ala Ala Gly Pro Ser Ala Asp Ser Val Thr Glu
 530 535 540

Asn Lys Ile Gly Ser Pro Pro Lys Thr Pro Val Ser Asn Val Ala Ala
 545 550 555 560

Thr Ser Ala Gly Pro Ser Asn Val Gly Thr Glu Leu Asn Ser Val Pro
 565 570 575

Gln Lys Ser Ser Pro Phe Leu Thr Arg Val Pro Val Tyr Pro Pro His
 580 585 590

Ser Glu Asn Ile Gln Tyr Phe Gln Asp Pro Arg Thr Gln Ile Pro Phe
 595 600 605

Glu Val Pro Gln Tyr Pro Gln Thr Gly Tyr Tyr Pro Pro Pro Pro Thr
 610 615 620

Val Pro Ala Gly Val Ala Pro Cys Val Pro Arg Phe Val Arg Ser Asn
 625 630 635 640

Asn Val Pro Glu Ser Ser Leu Pro Pro Ala Ser Met Pro Tyr Ala Asp
 645 650 655

His Tyr Ser Thr Phe Ser Pro Arg Asp Arg Met Asn Ser Ser Pro Tyr
 660 665 670

Gln Pro Pro Pro Pro Gln Pro Tyr Gly Pro Val Pro Pro Val Pro Ser
 675 680 685

Gly Met Tyr Ala Pro Val Tyr Asp Ser Arg Arg Ile Trp Arg Pro Pro
 690 695 700

Met Tyr Gln Arg Asp Asp Ile Ile Arg Ser Asn Ser Leu Pro Pro Met
 705 710 715 720

Asp Val Met His Ser Ser Val Tyr Gln Thr Ser Leu Arg Glu Arg Tyr
725 730 735

Asn Ser Leu Asp Gly Tyr Tyr Ser Val Ala Cys Gln Pro Pro Ser Glu
740 745 750

Pro Arg Thr Thr Val Pro Leu Pro Arg Glu Pro Cys Gly His Leu Lys
755 760 765

Thr Ser Cys Glu Glu Gln Ile Arg Arg Lys Pro Asp Gln Trp Ala Gln
770 775 780

Tyr His Thr Gln Lys Ala Pro Leu Val Ser Ser Thr Leu Pro Val Ala
785 790 795 800

Thr Gln Ser Pro Thr Pro Pro Ser Pro Leu Phe Ser Val Asp Phe Arg
805 810 815

Ala Asp Phe Ser Glu Ser Val Ser Gly Thr Lys Phe Glu Glu Asp His
820 825 830

Leu Ser His Tyr Ser Pro Trp Ser Cys Gly Thr Ile Gly Ser Cys Ile
835 840 845

Asn Ala Ile Asp Ser Glu Pro Lys Asp Val Ile Ala Asn Ser Asn Ala
850 855 860

Val Leu Met Asp Leu Asp Ser Gly Asp Val Lys Arg Arg Val His Leu
865 870 875 880

Phe Glu Thr Gln Arg Arg Thr Lys Glu Glu Asp Pro Ile Ile Pro Phe
885 890 895

Ser Asp Gly Pro Ile Ile Ser Lys Trp Gly Ala Ile Ser Arg Ser Ser
900 905 910

Arg Thr Gly Tyr His Thr Thr Asp Pro Val Gln Ala Thr Ala Ser Gln
915 920 925

Gly Ser Ala Thr Lys Pro Ile Ser Val Ser Asp Tyr Val Pro Tyr Val
930 935 940

Asn Ala Val Asp Ser Arg Trp Ser Ser Tyr Gly Asn Glu Ala Thr Ser
 945 950 955 960

Ser Ala His Tyr Val Glu Arg Asp Arg Phe Ile Val Thr Asp Leu Ser
 965 970 975

Gly His Arg Lys His Ser Ser Thr Gly Asp Leu Leu Ser Leu Glu Leu
 980 985 990

Gln Gln Ala Lys Ser Asn Ser Leu Leu Leu Gln Arg Glu Ala Asn Ala
 995 1000 1005

Leu Ala Met Gln Gln Lys Trp Asn Ser Leu Asp Glu Gly Arg His
 1010 1015 1020

Leu Thr Leu Asn Leu Leu Ser Lys Glu Ile Glu Leu Arg Asn Gly
 1025 1030 1035

Glu Leu Gln Ser Asp Tyr Thr Glu Asp Ala Thr Asp Thr Lys Pro
 1040 1045 1050

Asp Arg Asp Ile Glu Leu Glu Leu Ser Ala Leu Asp Thr Asp Glu
 1055 1060 1065

Pro Asp Gly Gln Ser Glu Pro Ile Glu Glu Ile Leu Asp Ile Gln
 1070 1075 1080

Leu Gly Ile Ser Ser Gln Asn Asp Gln Leu Leu Asn Gly Met Ala
 1085 1090 1095

Val Glu Asn Gly His Pro Val Gln Gln His Gln Lys Glu Pro Pro
 1100 1105 1110

Lys Gln Lys Lys Gln Ser Leu Gly Glu Asp His Val Ile Leu Glu
 1115 1120 1125

Glu Gln Lys Thr Ile Leu Pro Val Thr Ser Cys Phe Ser Gln Pro
 1130 1135 1140

Leu Pro Val Ser Ile Ser Asn Ala Ser Cys Leu Pro Ile Thr Thr
 1145 1150 1155

Ser Val Ser Ala Gly Asn Leu Ile Leu Lys Thr His Val Met Ser

1160

1165

1170

Glu Asp Lys Asn Asp Phe Leu Lys Pro Val Ala Asn Gly Lys Met
 1175 1180 1185

Val Asn Ser
 1190

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 <213> Artificial

<220>
 <223> PCR primer 1 for cloning DNA-R

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39

<210> 6
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 <212> DNA
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<220>
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 ggtatctaga tccatggtgt ggtcac

26

<210> 7
 <211> 574
 <212> PRT
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<400> 7

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Arg Gln Gly Ser Arg Gly Thr Ala Val Val Lys Val Leu Glu Cys Gly
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Val Cys Glu Asp Val Phe Ser Leu Gln Gly Asp Lys Val Pro Arg Leu
 35 40 45

Leu Leu Cys Gly His Thr Val Cys His Asp Cys Leu Thr Arg Leu Pro
 50 55 60

Leu His Gly Arg Ala Ile Arg Cys Pro Phe Asp Arg Gln Val Thr Asp
 65 70 75 80

Leu Gly Asp Ser Gly Val Trp Gly Leu Lys Lys Asn Phe Ala Leu Leu
 85 90 95
 Glu Leu Leu Glu Arg Leu Gln Asn Gly Pro Ile Gly Gln Tyr Gly Ala
 100 105 110
 Ala Glu Glu Ser Ile Gly Ile Ser Gly Glu Ser Ile Ile Arg Cys Asp
 115 120 125
 Glu Asp Glu Ala His Leu Ala Ser Val Tyr Cys Thr Val Cys Ala Thr
 130 135 140
 His Leu Cys Ser Glu Cys Ser Gln Val Thr His Ser Thr Lys Thr Leu
 145 150 155 160
 Ala Lys His Arg Arg Val Pro Leu Ala Asp Lys Pro His Glu Lys Thr
 165 170 175
 Met Cys Ser Gln His Gln Val His Ala Ile Glu Phe Val Cys Leu Glu
 180 185 190
 Glu Gly Cys Gln Thr Ser Pro Leu Met Cys Cys Val Cys Lys Glu Tyr
 195 200 205
 Gly Lys His Gln Gly His Lys His Ser Val Leu Glu Pro Glu Ala Asn
 210 215 220
 Gln Ile Arg Ala Ser Ile Leu Asp Met Ala His Cys Ile Arg Thr Phe
 225 230 235 240
 Thr Glu Glu Ile Ser Asp Tyr Ser Arg Lys Leu Val Gly Ile Val Gln
 245 250 255
 His Ile Glu Gly Gly Glu Gln Ile Val Glu Asp Gly Ile Gly Met Ala
 260 265 270
 His Thr Glu His Val Pro Gly Thr Ala Glu Asn Ala Arg Ser Cys Ile
 275 280 285
 Arg Ala Tyr Phe Tyr Asp Leu His Glu Thr Leu Cys Arg Gln Glu Glu
 290 295 300
 Met Ala Leu Ser Val Val Asp Ala His Val Arg Glu Lys Leu Ile Trp
 305 310 315 320
 Leu Arg Gln Gln Gln Glu Asp Met Thr Ile Leu Leu Ser Glu Val Ser
 325 330 335
 Ala Ala Cys Leu His Cys Glu Lys Thr Leu Gln Gln Asp Asp Cys Arg
 340 345 350
 Val Val Leu Ala Lys Gln Glu Ile Thr Arg Leu Leu Thr Glu Leu Gln
 355 360 365
 Lys Gln Gln Gln Gln Phe Thr Glu Val Ala Asp His Ile Gln Leu Asp
 370 375 380

Ala Ser Ile Pro Val Thr Phe Thr Lys Asp Asn Arg Val His Ile Gly
385 390 395 400

Pro Lys Met Glu Ile Arg Val Val Thr Leu Gly Leu Asp Gly Ala Gly
405 410 415

Lys Thr Thr Ile Leu Phe Lys Leu Lys Gln Asp Glu Phe Met Gln Pro
420 425 430

Ile Pro Thr Ile Gly Phe Asn Val Glu Thr Val Glu Tyr Lys Asn Leu
435 440 445

Lys Phe Thr Ile Trp Asp Val Gly Gly Lys His Lys Leu Arg Pro Leu
450 455 460

Trp Lys His Tyr Tyr Leu Asn Thr Gln Ala Val Val Phe Val Val Asp
465 470 475 480

Ser Ser His Arg Asp Arg Ile Ser Glu Ala His Ser Glu Leu Ala Lys
485 490 495

Leu Leu Thr Glu Lys Glu Leu Arg Asp Ala Leu Leu Leu Ile Phe Ala
500 505 510

Asn Lys Gln Asp Val Ala Gly Ala Leu Ser Val Glu Glu Ile Thr Glu
515 520 525

Leu Leu Ser Leu His Lys Leu Cys Cys Gly Arg Ser Trp Tyr Ile Gln
530 535 540

Gly Cys Asp Ala Arg Ser Gly Met Gly Leu Tyr Glu Gly Leu Asp Trp
545 550 555 560

Leu Ser Arg Gln Leu Val Ala Ala Gly Val Leu Asp Val Ala
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<210> 8

<211> 317

<212> PRT

<213> Homo sapiens

<400> 8

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His Cys Glu His Ala Phe Cys Asn Ala Cys Ile Thr Gln Trp Phe Ser
35 40 45

Gln Gln Gln Thr Cys Pro Val Asp Arg Ser Val Val Thr Val Ala His
50 55 60

Leu Arg Pro Val Pro Arg Ile Met Arg Asn Met Leu Ser Lys Leu Gln
65 70 75 80

Ile Ala Cys Asp Asn Ala Val Phe Gly Cys Ser Ala Val Val Arg Leu
 85 90 95
 Asp Asn Leu Met Ser His Leu Ser Asp Cys Glu His Asn Pro Lys Arg
 100 105 110
 Pro Val Thr Cys Glu Gln Gly Cys Gly Leu Glu Met Pro Lys Asp Glu
 115 120 125
 Leu Pro Asn His Asn Cys Ile Lys His Leu Arg Ser Val Val Gln Gln
 130 135 140
 Gln Gln Thr Arg Ile Ala Glu Leu Glu Lys Thr Ser Ala Glu His Lys
 145 150 155 160
 His Gln Leu Ala Glu Gln Lys Arg Asp Ile Gln Leu Leu Lys Ala Tyr
 165 170 175
 Met Arg Ala Ile Arg Ser Val Asn Pro Asn Leu Gln Asn Leu Glu Glu
 180 185 190
 Thr Ile Glu Tyr Asn Glu Ile Leu Glu Trp Val Asn Ser Leu Gln Pro
 195 200 205
 Ala Arg Val Thr Arg Trp Gly Gly Met Ile Ser Thr Pro Asp Ala Val
 210 215 220
 Leu Gln Ala Val Ile Lys Arg Ser Leu Val Glu Ser Gly Cys Pro Ala
 225 230 235 240
 Ser Ile Val Asn Glu Leu Ile Glu Asn Ala His Glu Arg Ser Trp Pro
 245 250 255
 Gln Gly Leu Ala Thr Leu Glu Thr Arg Gln Met Asn Arg Arg Tyr Tyr
 260 265 270
 Glu Asn Tyr Val Ala Lys Arg Ile Pro Gly Lys Gln Ala Val Val Val
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 Gly Leu Val Met Ile Phe Ala His Gly Val Glu Glu Ile
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 <211> 202
 <212> PRT
 <213> Caenorhabditis elegans

<400> 9

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 35 40 45
 Thr Glu Arg Lys Leu Ala Lys Thr Ser Ala Glu Leu Lys Ala Lys Asp
 50 55 60
 Glu Lys Leu Lys Lys Glu Thr Ala Ser Leu Glu Ala Ser Arg Glu Ala
 65 70 75 80
 His Arg Leu Leu Gln Glu Glu Ser Asn Lys Ser Lys Val Ser Val Met
 85 90 95
 Arg Leu Thr Phe Lys Leu Asn Arg Ile Thr His Glu Ser Val Lys Glu
 100 105 110
 Gln Ala Val Leu Lys Lys Lys Leu Leu Asp Cys Glu Thr Arg Leu Ala
 115 120 125
 Thr Tyr Ser Glu Cys Leu Val Cys Tyr Gln Lys Phe Asp Glu Asn Thr
 130 135 140
 Arg Ile Pro Arg Val Met Asp Cys Gly His Thr Leu Cys Asp Phe Cys
 145 150 155 160
 Ile Asn Gln Ile Val Lys Met Ala Gly Cys Tyr Ser Ala Thr Cys Pro
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 180 185 190
 Asp Arg Pro Cys Asn Arg Phe Ile Met Lys
 195 200

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 <211> 218
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 <213> Caenorhabditis elegans

 <400> 10

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 20 25 30
 Ala Glu Glu Glu Gln Phe Ser Asp Lys Met Lys Gln Leu Glu Asp Glu
 35 40 45
 Ile Lys Ile Lys Glu Gln Val Ile Thr Met Phe Lys Arg Lys Thr Val
 50 55 60
 Arg Arg Glu Trp Met Arg Asn Ser Arg Gln Ala Thr Thr Asn Ile Asn
 65 70 75 80

Ile Ala Gln Ile Glu Ser Leu Lys Leu Gln Leu Glu Glu Gly Glu Lys
85 90 95

Asp Ile Ala Glu Ala Glu Lys Gln Ala Glu Pro Thr Thr Pro Gln Gln
100 105 110

Glu Ala Glu Leu Ser Glu Thr Phe Lys Gln Met Val Arg Asp Arg Met
115 120 125

Lys Val Lys Asp Val Asp Glu Lys Leu Leu Gln Gln Tyr Met Lys Lys
130 135 140

Glu Asn Val Glu Phe Glu Trp Arg Ser Cys Phe Ile Cys Thr Met Glu
145 150 155 160

Tyr Ser Arg Thr Asp Lys Asn Leu His Pro Ile Ile Leu Asn Cys Gly
165 170 175

His Asn Leu Cys Arg Ser Cys Ile Asn Lys Leu Thr Gly Asn Gly Ile
180 185 190

Val Lys Cys Pro Phe Asp Arg Leu Asp Thr Arg Val Arg Val Thr Gly
195 200 205

Leu Pro Arg Asn Leu Ala Leu Ile Asn Leu
210 215

<210> 11

<211> 1048

<212> PRT

<213> Caenorhabditis elegans

<400> 11

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20 25 30

Ile Cys Gly His Val Ile Cys Arg Lys Cys Ala Glu Lys Pro Glu Asn
35 40 45

Gln Thr Lys Pro Cys Pro His Asp Asp Trp Lys Thr Thr His Ser Pro
50 55 60

Ser Glu Tyr Pro Asn Asn Val Ala Leu Leu Ser Val Ile Phe Pro Arg
65 70 75 80

Lys Gln Cys Met Thr Leu Ser Gly Ala Val Ser Glu Ala Glu Lys Arg
85 90 95

Val Asp Gln Leu Ser Ile Gln Ile Ala Lys Phe Phe Arg Glu Ala Asp
100 105 110

Ser Glu Arg Gly Gly Thr Val Ser Ser Arg Glu Ile Ser Arg Thr Leu
115 120 125

Gln Arg Lys Val Leu Ala Leu Leu Cys Tyr Gln Trp Arg Glu Val Asp
 130 135 140
 Gly Arg Leu Lys Thr Leu Lys Met Cys Arg Gly Ile Ser Glu Arg Val
 145 150 155 160
 Met Ile Glu Ile Ile Leu Ser Ile Gln Ser Asn Thr His Val Ser Ser
 165 170 175
 Gln Leu Trp Ser Ala Val Arg Ala Arg Gly Cys Gln Phe Leu Gly Pro
 180 185 190
 Ala Met Gln Asp Asp Val Leu Arg Leu Ile Leu Met Thr Leu Glu Thr
 195 200 205
 Gly Glu Cys Ile Ala Arg Lys Asn Leu Val Met Tyr Val Val Gln Thr
 210 215 220
 Leu Ala Ser Asp Tyr Pro Gln Val Ser Lys Thr Cys Val Gly His Val
 225 230 235 240
 Val Gln Leu Leu Tyr Arg Ala Ser Cys Phe Asn Val Leu Lys Arg Asp
 245 250 255
 Gly Glu Ser Ser Leu Met Gln Leu Lys Glu Glu Phe Arg Thr Tyr Glu
 260 265 270
 Ser Leu Arg Arg Glu His Asp Ser Gln Ile Val Gln Ile Ala Phe Glu
 275 280 285
 Ser Gly Leu Arg Ile Gly Pro Asp Gln Trp Ser Ala Leu Leu Tyr Ala
 290 295 300
 Asp Gln Ser His Arg Ser His Met Gln Ser Ile Ile Asp Lys Leu Gln
 305 310 315 320
 Ser Lys Asn Ser Tyr Gln Gln Gly Val Glu Glu Leu Arg Ala Leu Ala
 325 330 335
 Gly Ser Gln Thr Ser Met Leu Val Pro Ala Tyr Arg Tyr Phe Leu Thr
 340 345 350
 Gln Val Ile Pro Cys Leu Glu Phe Phe Ala Gly Ile Glu His Glu Asp
 355 360 365
 Thr Ser Met Arg Met Ile Gly Asp Ala Leu His Gln Ile Arg Ile Leu
 370 375 380
 Leu Lys Leu His Cys Ser Gln Asp Asp Leu Arg Lys Met Pro Lys Glu
 385 390 395 400
 Glu Arg Arg Gly Val Ile Leu Gln Ala Glu Val Pro Gly Gly Met Gly
 405 410 415
 Gly Gly Pro Gly Gly Ser Gly Gly Ala Glu Ala Gly Arg Ile Gly Gly
 420 425 430

Leu His Pro Leu Tyr Ser Gln Ile Asp Glu Thr Gly Arg Ser Ile Ser
 435 440 445

Arg Thr Asn Pro Lys Asp Asn Ser His Asn Ser Pro Gln Thr Pro Pro
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Lys Gln Pro Arg Gln Lys Arg Tyr Gln Met Gly Ile Pro Pro Asn Arg
 465 470 475 480

Met Gly Tyr Ser Ser Asp Ala Pro Pro Phe Ile Pro Ser His Gln Gln
 485 490 495

Gln Pro Pro Pro Gln Phe Phe Asn Ser Gln His Leu Pro Gln Arg Phe
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Arg Gly Gly Arg Gln Arg Gly Ala Pro Pro Pro Pro Pro Gln Pro
 515 520 525

Met Pro Met Leu Ile Gly Tyr Asp Met Pro Gly Ala Pro Met Met Gln
 530 535 540

Ala Thr Glu Val Leu Thr Ala Asp Gly Gln Met Val Asn Gly Thr Pro
 545 550 555 560

Gln Arg Val Val Ile Met Gln Ser Pro Thr His Leu Pro Gly Gly Pro
 565 570 575

Val Val Met Ile Pro Gln Gln Gln Met Val Pro Pro Pro Gln Ser Met
 580 585 590

Thr Pro Val Gly Gly Pro Met Gly Pro Met Gly Pro Met Thr Pro Ser
 595 600 605

Ile Pro Val Gln Val Pro Pro Asn Thr Met Trp Thr Ala Thr Ser Pro
 610 615 620

Thr Gly Ser Val Ile Tyr Pro Ala Ala Ser Pro Pro Gly Gln Pro Pro
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His Thr Ile Trp Ile Gln Ser Ile Gly Val Phe Lys Arg Lys Ser Asn
 645 650 655

Phe Leu Lys Ile Val Arg Lys Ile Ser Phe Phe Leu Asn Phe Tyr Asp
 660 665 670

Phe Phe Leu Ile Leu Arg Lys Leu Lys Lys Glu Lys Lys Gly Ala Asp
 675 680 685

Ile Glu Phe Phe Glu Lys Ile Lys Ser Thr Asp Phe Lys Lys Tyr Pro
 690 695 700

Ser Ser Phe Ser Arg Thr Asp Gly Asn Met Phe Pro Met Phe Asp Arg
 705 710 715 720

Gly Ser Gly Gly Met Val Trp Gly Pro Gly Thr Met Leu Arg Glu Ser
 725 730 735

Gly Ala Asp Ala Glu Gln Leu Leu Ala Lys Arg Tyr Glu Ile Leu Lys
 740 745 750
 Arg Leu Gln Pro Ser Glu Asp Asp Asp Asp Pro Glu Asp Gly Gly Ile
 755 760 765
 Gly His Val Ser Tyr Thr Val Ala Ser Ser Val Leu Asp Asp Arg Met
 770 775 780
 Asp His His Pro Leu Thr Met Ile Pro Val Pro Thr Ile Asp Leu Pro
 785 790 795 800
 Ala Ile Pro Ile Ser Phe Ala Asn Met Pro Thr Glu Glu Thr Met Thr
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 Met Ile Gly Glu Met Val Gln Asn Arg Pro Arg Ala Pro Ser Leu Thr
 820 825 830
 Ala Pro Ser Ser Asn Gln Pro Met Asn Val Asn Ala Ser Ala Ser Ala
 835 840 845
 Thr Val Gln Ala Glu Cys Glu Asn Arg Lys Ile Leu Asp Phe Pro Leu
 850 855 860
 Lys Tyr Arg Lys Met Thr Leu Met Phe Glu Lys Val Ser Thr Cys Phe
 865 870 875 880
 His Val Thr Leu Leu Lys Asp Tyr Met Val Phe Tyr Val Leu Asn Thr
 885 890 895
 Leu Asn Phe Ala Ser Arg Trp Pro Arg Arg Arg Arg Ala Ala Thr Ile
 900 905 910
 Pro Gln Pro Val Ile Pro Met Val Gln Val Pro Val Gln Val Pro Ile
 915 920 925
 Val Pro Ala Glu Asn Phe Asn Pro Asn Val Pro Pro Pro Pro Pro
 930 935 940
 Pro Gln Gly Gln Pro Met Leu Val Asp Ser Ala Ile Gly Leu Leu Thr
 945 950 955 960
 Pro Ile Arg Pro Ile Leu Val Ala His Pro Gln Asn Val Val Ser Asn
 965 970 975
 Ser Leu Asp Lys Ile Val Asp Val Lys Glu Arg Ile Ser Glu Ala Gln
 980 985 990
 Gly Asn Ala Ser Glu Ala Glu Asn Ala His Leu Arg Met Glu Leu Arg
 995 1000 1005
 Met Ala Glu Ser Gln Met Ala His Leu Asp Pro Tyr Thr Lys Asn
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Gln Leu His Leu Asn Pro Thr Val Glu Gly
1040 1045

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<212> DNA
<213> Homo sapiens

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<221> CDS
<222> (86)..(1498)

<400> 12

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                               Met Pro Gly Phe Asp Tyr Lys Phe Leu
                               1                               5

gag aag ccc aag cga cgg ctg ctg tgc cca ctg tgc ggg aag ccc atg      160
Glu Lys Pro Lys Arg Arg Leu Leu Cys Pro Leu Cys Gly Lys Pro Met
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cgc gag cct gtg cag gtt tcc acc tgc ggc cac cgt ttc tgc gat acc      208
Arg Glu Pro Val Gln Val Ser Thr Cys Gly His Arg Phe Cys Asp Thr
                               30                               35                               40

tgc ctg cag gag ttc ctc agt gaa gga gtc ttc aag tgc cct gag gac      256
Cys Leu Gln Glu Phe Leu Ser Glu Gly Val Phe Lys Cys Pro Glu Asp
                               45                               50                               55

cag ctt cct ctg gac tat gcc aag atc tac cca gac ccg gag ctg gaa      304
Gln Leu Pro Leu Asp Tyr Ala Lys Ile Tyr Pro Asp Pro Glu Leu Glu
60                               65                               70

gta caa gta ttg ggc ctg cct atc cgc tgc atc cac agt gag gag ggc      352
Val Gln Val Leu Gly Leu Pro Ile Arg Cys Ile His Ser Glu Glu Gly
75                               80                               85

tgc cgc tgg agt ggg cca cta cgt cat cta cag ggc cac ctg aat acc      400
Cys Arg Trp Ser Gly Pro Leu Arg His Leu Gln Gly His Leu Asn Thr
90                               95                               100                               105

tgc agc ttc aat gtc att ccc tgc cct aat cgc tgc ccc atg aag ctg      448
Cys Ser Phe Asn Val Ile Pro Cys Pro Asn Arg Cys Pro Met Lys Leu
110                               115                               120

agc cgc cgt gat cta cct gca cac ttg cag cat gac tgc ccc aag cgg      496
Ser Arg Arg Asp Leu Pro Ala His Leu Gln His Asp Cys Pro Lys Arg
125                               130                               135

cgc ctc aag tgc gag ttt tgt ggc tgt gac ttc agt ggg gag gcc tat      544
Arg Leu Lys Cys Glu Phe Cys Gly Cys Asp Phe Ser Gly Glu Ala Tyr
140                               145                               150

gag agc cat gag ggt atg tgc ccc cag gag agt gtc tac tgt gag aat      592

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Glu Ser His Glu Gly Met Cys Pro Gln Glu Ser Val Tyr Cys Glu Asn	
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Lys Cys Gly Ala Arg Met Met Arg Gly Leu Leu Ala Gln His Ala Thr	
170	175 180 185
tct gag tgc ccc aag cgc act cag ccc tgc acc tac tgc act aag gag	688
Ser Glu Cys Pro Lys Arg Thr Gln Pro Cys Thr Tyr Cys Thr Lys Glu	
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ttc gtc ttt gac acc atc cag agc cac cag tac cag tgc cca agg ctg	736
Phe Val Phe Asp Thr Ile Gln Ser His Gln Tyr Gln Cys Pro Arg Leu	
	205 210 215
cct gtt gcc tgc ccc aac caa tgt ggt gtg ggc act gtg gct cgg gag	784
Pro Val Ala Cys Pro Asn Gln Cys Gly Val Gly Thr Val Ala Arg Glu	
	220 225 230
gac ctg cca ggc cat ctg aag gac agc tgt aac acc gcc ctg gtg ctc	832
Asp Leu Pro Gly His Leu Lys Asp Ser Cys Asn Thr Ala Leu Val Leu	
	235 240 245
tgc cca ttc aaa gac tcc ggc tgc aag cac agg tgc cct aag ctg gca	880
Cys Pro Phe Lys Asp Ser Gly Cys Lys His Arg Cys Pro Lys Leu Ala	
	250 255 260 265
atg gca cgg cat gtg gag gag agt gtg aag cca cat ctg gcc atg atg	928
Met Ala Arg His Val Glu Glu Ser Val Lys Pro His Leu Ala Met Met	
	270 275 280
tgt gcc ctg gtg agc cgg caa cgg cag gag ctg cag gag ctt cgg cga	976
Cys Ala Leu Val Ser Arg Gln Arg Gln Glu Leu Gln Glu Arg Arg	
	285 290 295
gag ctg gag gag cta tca gtg ggc agt gat ggc gtg ctc atc tgg aag	1024
Glu Leu Glu Glu Leu Ser Val Gly Ser Asp Gly Val Leu Ile Trp Lys	
	300 305 310
att ggc agc tat gga cgg cgg cta cag gag gcc aag gcc aag ccc aac	1072
Ile Gly Ser Tyr Gly Arg Arg Leu Gln Glu Ala Lys Ala Lys Pro Asn	
	315 320 325
ctt gag tgc ttc agc cca gcc ttc tac aca cat aag tat ggt tac aag	1120
Leu Glu Cys Phe Ser Pro Ala Phe Tyr Thr His Lys Tyr Gly Tyr Lys	
	330 335 340 345
ctg cag gtg tct gca ttc ctc aat ggc aat ggc agt ggt gag ggc aca	1168
Leu Gln Val Ser Ala Phe Leu Asn Gly Asn Gly Ser Gly Glu Gly Thr	
	350 355 360
cac ctc tca ctg tac att cgt gtg ctg cct ggt gcc ttt gac aat ctc	1216
His Leu Ser Leu Tyr Ile Arg Val Leu Pro Gly Ala Phe Asp Asn Leu	
	365 370 375
ctt gag tgg ccc ttt gcc cgc cgt gtc acc ttc tcc ctg ctg gat cag	1264
Leu Glu Trp Pro Phe Ala Arg Arg Val Thr Phe Ser Leu Leu Asp Gln	

380	385	390	
agc gac cct ggg ctg gct aaa cca cag cac gtc act gag acc ttc cac			1312
Ser Asp Pro Gly Leu Ala Lys Pro Gln His Val Thr Glu Thr Phe His			
395	400	405	
ccc gac cca aac tgg aag aat ttc cag aag cca ggc acg tgg cgg ggc			1360
Pro Asp Pro Asn Trp Lys Asn Phe Gln Lys Pro Gly Thr Trp Arg Gly			
410	415	420	425
tcc ctg gat gag agt tct ctg ggc ttt ggt tat ccc aag ttc atc tcc			1408
Ser Leu Asp Glu Ser Ser Leu Gly Phe Gly Tyr Pro Lys Phe Ile Ser			
	430	435	440
cac cag gac att cga aag cga aac tat gtg cgg gat gat gca gtc ttc			1456
His Gln Asp Ile Arg Lys Arg Asn Tyr Val Arg Asp Asp Ala Val Phe			
	445	450	455
atc cgt gct gct gtt gaa ctg ccc cgg aag atc ctc agc tga			1498
Ile Arg Ala Ala Val Glu Leu Pro Arg Lys Ile Leu Ser			
	460	465	470
gtgcaggtgg ggttcgaggg gaaaggacga tggggcatga cctcagtcag gcactggctg			1558
aacttggaga gggggccgga cccccgtcag ctgcttctgc tgccntaggtt ctgttaccce			1618
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gcctgctcag gtgctatgtc ccaagagcca taagggggtg ggaattgggg agggagaaag			1858
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<210> 13
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 <212> PRT
 <213> Homo sapiens

<400> 13

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			20					25						30	

Thr Cys Gly His Arg Phe Cys Asp Thr Cys Leu Gln Glu Phe Leu Ser

35

40

45

Glu Gly Val Phe Lys Cys Pro Glu Asp Gln Leu Pro Leu Asp Tyr Ala
50 55 60

Lys Ile Tyr Pro Asp Pro Glu Leu Glu Val Gln Val Leu Gly Leu Pro
65 70 75 80

Ile Arg Cys Ile His Ser Glu Glu Gly Cys Arg Trp Ser Gly Pro Leu
85 90 95

Arg His Leu Gln Gly His Leu Asn Thr Cys Ser Phe Asn Val Ile Pro
100 105 110

Cys Pro Asn Arg Cys Pro Met Lys Leu Ser Arg Arg Asp Leu Pro Ala
115 120 125

His Leu Gln His Asp Cys Pro Lys Arg Arg Leu Lys Cys Glu Phe Cys
130 135 140

Gly Cys Asp Phe Ser Gly Glu Ala Tyr Glu Ser His Glu Gly Met Cys
145 150 155 160

Pro Gln Glu Ser Val Tyr Cys Glu Asn Lys Cys Gly Ala Arg Met Met
165 170 175

Arg Gly Leu Leu Ala Gln His Ala Thr Ser Glu Cys Pro Lys Arg Thr
180 185 190

Gln Pro Cys Thr Tyr Cys Thr Lys Glu Phe Val Phe Asp Thr Ile Gln
195 200 205

Ser His Gln Tyr Gln Cys Pro Arg Leu Pro Val Ala Cys Pro Asn Gln
210 215 220

Cys Gly Val Gly Thr Val Ala Arg Glu Asp Leu Pro Gly His Leu Lys
225 230 235 240

Asp Ser Cys Asn Thr Ala Leu Val Leu Cys Pro Phe Lys Asp Ser Gly
245 250 255

Cys Lys His Arg Cys Pro Lys Leu Ala Met Ala Arg His Val Glu Glu
260 265 270

Ser Val Lys Pro His Leu Ala Met Met Cys Ala Leu Val Ser Arg Gln
275 280 285

Arg Gln Glu Leu Gln Glu Leu Arg Arg Glu Leu Glu Glu Leu Ser Val
290 295 300

Gly Ser Asp Gly Val Leu Ile Trp Lys Ile Gly Ser Tyr Gly Arg Arg
305 310 315 320

Leu Gln Glu Ala Lys Ala Lys Pro Asn Leu Glu Cys Phe Ser Pro Ala
325 330 335

Phe Tyr Thr His Lys Tyr Gly Tyr Lys Leu Gln Val Ser Ala Phe Leu
340 345 350

Asn Gly Asn Gly Ser Gly Glu Gly Thr His Leu Ser Leu Tyr Ile Arg
355 360 365

Val Leu Pro Gly Ala Phe Asp Asn Leu Leu Glu Trp Pro Phe Ala Arg
370 375 380

Arg Val Thr Phe Ser Leu Leu Asp Gln Ser Asp Pro Gly Leu Ala Lys
385 390 395 400

Pro Gln His Val Thr Glu Thr Phe His Pro Asp Pro Asn Trp Lys Asn
405 410 415

Phe Gln Lys Pro Gly Thr Trp Arg Gly Ser Leu Asp Glu Ser Ser Leu
420 425 430

Gly Phe Gly Tyr Pro Lys Phe Ile Ser His Gln Asp Ile Arg Lys Arg
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Asn Tyr Val Arg Asp Asp Ala Val Phe Ile Arg Ala Ala Val Glu Leu
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Pro Arg Lys Ile Leu Ser
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<210> 14
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<212> DNA

<213> Caenorhabditis elegans

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<222> (10)..(1017)

<400> 14

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aac aac tca gat gac acg tcg ttc gct gcc gat cga tcg aac agt ctt      99
Asn Asn Ser Asp Asp Thr Ser Phe Ala Ala Asp Arg Ser Asn Ser Leu
15              20              25              30

ctg aat gcg acg tgc ccg gcg aga att caa aat tca gta gat caa cgg      147
Leu Asn Ala Thr Cys Pro Ala Arg Ile Gln Asn Ser Val Asp Gln Arg
      35              40              45

aaa atc aat cga tca ttc aat gat tcg ctg tcg tcc gga tat agt gga      195
Lys Ile Asn Arg Ser Phe Asn Asp Ser Leu Ser Ser Gly Tyr Ser Gly
      50              55              60

aaa tgg ctt cgt cca aag cgt gaa gcg ctc aag atc act cca ttg gct      243
Lys Trp Leu Arg Pro Lys Arg Glu Ala Leu Lys Ile Thr Pro Leu Ala
      65              70              75

cag att gac gag gcg ccg gca act aaa aga cat agc tcg gcg aag gat      291
Gln Ile Asp Glu Ala Pro Ala Thr Lys Arg His Ser Ser Ala Lys Asp
      80              85              90

aag cac aca gaa tac aaa acg cga ctt tgt gat gcg ttc cgc cgt gaa      339
Lys His Thr Glu Tyr Lys Thr Arg Leu Cys Asp Ala Phe Arg Arg Glu
95              100              105              110

gga tac tgc ccg tac aac gac aat tgc aca tat gct cac gga caa gat      387
Gly Tyr Cys Pro Tyr Asn Asp Asn Cys Thr Tyr Ala His Gly Gln Asp
      115              120              125

gag ctg aga gtt ccg aga cgc cgc caa gag tat tat tcc cga gat cca      435
Glu Leu Arg Val Pro Arg Arg Arg Gln Glu Tyr Tyr Ser Arg Asp Pro
      130              135              140

cca cgt gag cgc cgt gat tct cgt tct aga cga gac gac gtg gat aca      483
Pro Arg Glu Arg Arg Asp Ser Arg Ser Arg Arg Asp Asp Val Asp Thr
145              150              155

aca atc aat cga tcg agt tct tca gca tcg aag cat cat gat gag aat      531
Thr Ile Asn Arg Ser Ser Ser Ser Ala Ser Lys His His Asp Glu Asn
160              165              170

cgg aga ccc agc aac aac cac gga agc tcg aat cgt cgt cag att tgt      579
Arg Arg Pro Ser Asn Asn His Gly Ser Ser Asn Arg Arg Gln Ile Cys
175              180              185              190

cac aat ttc gag aga gga aac tgc aga tat ggt cca aga tgc cgc ttc      627
His Asn Phe Glu Arg Gly Asn Cys Arg Tyr Gly Pro Arg Cys Arg Phe
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195	200	205	
att cac gtc gaa caa atg caa cat ttc aat gcg aat gcg acg gtt tac Ile His Val Glu Gln Met Gln His Phe Asn Ala Asn Ala Thr Val Tyr 210 215 220			675
gcg cca cct tct tcc gat tgt ccg ccg ccg att gcc tac tac cat cat Ala Pro Pro Ser Ser Asp Cys Pro Pro Pro Ile Ala Tyr Tyr His His 225 230 235			723
cat cca caa cat cag caa caa ttc ctg cca ttt cca atg cca tat ttc His Pro Gln His Gln Gln Gln Phe Leu Pro Phe Pro Met Pro Tyr Phe 240 245 250			771
ttg gct cca ccg ccg caa gct caa caa gga gct cct ttt cca gtg caa Leu Ala Pro Pro Pro Gln Ala Gln Gln Gly Ala Pro Phe Pro Val Gln 255 260 265 270			819
tat att cca cag caa cat gat ttg atg aat agc cag cca atg tat gca Tyr Ile Pro Gln Gln His Asp Leu Met Asn Ser Gln Pro Met Tyr Ala 275 280 285			867
cca atg gca ccg aca tac tac tat caa cca att aat tcg aat ggc atg Pro Met Ala Pro Thr Tyr Tyr Tyr Gln Pro Ile Asn Ser Asn Gly Met 290 295 300			915
ccc atg atg gat gtg act att gat ccg aat gcc acg ggc ggt gcg ttt Pro Met Met Asp Val Thr Ile Asp Pro Asn Ala Thr Gly Gly Ala Phe 305 310 315			963
gaa gtg ttc ccc gat gga ttc ttc tct cag cca cca cca act att att Glu Val Phe Pro Asp Gly Phe Phe Ser Gln Pro Pro Pro Thr Ile Ile 320 325 330			1011
tcc taa ttttgccgta ttttccatat tttgttttgt atatttatcc actcaccgcc Ser 335			1067
tctctttgtc ctgtgaatga acttgtgcc aaaaagcc			1105

<210> 15
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 <212> PRT
 <213> Caenorhabditis elegans

<400> 15

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Ser	Asp	Asp	Thr	Ser	Phe	Ala	Ala	Asp	Arg	Ser	Asn	Ser	Leu	Leu	Asn
	20							25					30		

Ala Thr Cys Pro Ala Arg Ile Gln Asn Ser Val Asp Gln Arg Lys Ile

Asn Arg Ser Phe Asn Asp Ser Leu Ser Ser Gly Tyr Ser Gly Lys Trp
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Leu Arg Pro Lys Arg Glu Ala Leu Lys Ile Thr Pro Leu Ala Gln Ile
65 70 75 80

Asp Glu Ala Pro Ala Thr Lys Arg His Ser Ser Ala Lys Asp Lys His
85 90 95

Thr Glu Tyr Lys Thr Arg Leu Cys Asp Ala Phe Arg Arg Glu Gly Tyr
100 105 110

Cys Pro Tyr Asn Asp Asn Cys Thr Tyr Ala His Gly Gln Asp Glu Leu
115 120 125

Arg Val Pro Arg Arg Arg Gln Glu Tyr Tyr Ser Arg Asp Pro Pro Arg
130 135 140

Glu Arg Arg Asp Ser Arg Ser Arg Arg Asp Asp Val Asp Thr Thr Ile
145 150 155 160

Asn Arg Ser Ser Ser Ser Ala Ser Lys His His Asp Glu Asn Arg Arg
165 170 175

Pro Ser Asn Asn His Gly Ser Ser Asn Arg Arg Gln Ile Cys His Asn
180 185 190

Phe Glu Arg Gly Asn Cys Arg Tyr Gly Pro Arg Cys Arg Phe Ile His
195 200 205

Val Glu Gln Met Gln His Phe Asn Ala Asn Ala Thr Val Tyr Ala Pro
210 215 220

Pro Ser Ser Asp Cys Pro Pro Pro Ile Ala Tyr Tyr His His His Pro
225 230 235 240

Gln His Gln Gln Gln Phe Leu Pro Phe Pro Met Pro Tyr Phe Leu Ala
245 250 255

Pro Pro Pro Gln Ala Gln Gln Gly Ala Pro Phe Pro Val Gln Tyr Ile
260 265 270

Pro Gln Gln His Asp Leu Met Asn Ser Gln Pro Met Tyr Ala Pro Met
 275 280 285

Ala Pro Thr Tyr Tyr Tyr Gln Pro Ile Asn Ser Asn Gly Met Pro Met
 290 295 300

Met Asp Val Thr Ile Asp Pro Asn Ala Thr Gly Gly Ala Phe Glu Val
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Phe Pro Asp Gly Phe Phe Ser Gln Pro Pro Pro Thr Ile Ile Ser
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 <213> Drosophila melanogaster

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 gaaaagaaaa acaaaacgaa aaaattcgca ctttttttct gtcttgtcca gtggaaaata 240
 caacaaataa acaacaacgg ctaaatacaag ttaacaatct gttcaaaacc aatcaacaaa 300
 atg tct gct gat att ctg cag aaa tca aga gag cag gat gat tgc cac 348
 Met Ser Ala Asp Ile Leu Gln Lys Ser Arg Glu Gln Asp Asp Ser His
 1 5 10 15
 tac ttc gag cgt ggc gat ata tcc aaa tac gta acg atg aac gat cac 396
 Tyr Phe Glu Arg Gly Asp Ile Ser Lys Tyr Val Thr Met Asn Asp His
 20 25 30
 ttg ggt gat ttc gat tgc aac gag gtg cgc aag gaa ata agg atg ctg 444
 Leu Gly Asp Phe Asp Cys Asn Glu Val Arg Lys Glu Ile Arg Met Leu
 35 40 45
 ctc gcc cac ggc gcc aac ttg gat cag cag cac cag cag cag cca cat 492
 Leu Ala His Gly Ala Asn Leu Asp Gln Gln His Gln Gln Gln Pro His
 50 55 60
 cgc cac cat ggc ggt ctc aca cgc acc att tca cag ccg gcc cag ctc 540
 Arg His His Gly Gly Leu Thr Arg Thr Ile Ser Gln Pro Ala Gln Leu
 65 70 75 80

atc cag cag cag cag cag caa cac caa cag cag cag cag cag cag cag	588
Ile Gln Gln Gln Gln Gln Gln His Gln Gln Gln Gln Gln Gln Gln Gln	
85 90 95	
cca cct gtt gcc agt ctg gtg acc atc acc gag aac ctg ggc aac atg	636
Pro Pro Val Ala Ser Leu Val Thr Ile Thr Glu Asn Leu Gly Asn Met	
100 105 110	
aac ctg cac cga aag ctg gag cga acc caa tcg gag cca ctg ccg cca	684
Asn Leu His Arg Lys Leu Glu Arg Thr Gln Ser Glu Pro Leu Pro Pro	
115 120 125	
cag cag ccg atg aac aca tcc aga tac aag acc gag ctg tgc cgt ccg	732
Gln Gln Pro Met Asn Thr Ser Arg Tyr Lys Thr Glu Leu Cys Arg Pro	
130 135 140	
ttc gag gag gcc gga gaa tgc aag tac ggc gag aag tgc cag ttc gcc	780
Phe Glu Glu Ala Gly Glu Cys Lys Tyr Gly Glu Lys Cys Gln Phe Ala	
145 150 155 160	
cat gga agc cat gag ttg cga aac gtg cac cgt cat ccc aag tac aag	828
His Gly Ser His Glu Leu Arg Asn Val His Arg His Pro Lys Tyr Lys	
165 170 175	
acg gaa tac tgc cgc acc ttc cac agc gtg ggc ttc tgt ccc tac gga	876
Thr Glu Tyr Cys Arg Thr Phe His Ser Val Gly Phe Cys Pro Tyr Gly	
180 185 190	
ccg cgc tgt cac ttt gtt cac aat gcg gac gag gcc cgc gcc caa cag	924
Pro Arg Cys His Phe Val His Asn Ala Asp Glu Ala Arg Ala Gln Gln	
195 200 205	
gcg gcc cag gca gcc aag tcc tcc acc cag tcg cag tcg cag tcg cag	972
Ala Ala Gln Ala Ala Lys Ser Ser Thr Gln Ser Gln Ser Gln Ser Gln	
210 215 220	
cag tcg tcg tcg cag aac ttc tcg ccg aag agc aac cag agc agc aat	1020
Gln Ser Ser Ser Gln Asn Phe Ser Pro Lys Ser Asn Gln Ser Ser Asn	
225 230 235 240	
caa agt agc aac agt agc agc agc agc agc agc agc ggc ggc ggc ggt	1068
Gln Ser Ser Asn Ser Ser Ser Ser Ser Ser Ser Ser Gly Gly Gly Gly	
245 250 255	
ggc ggc ggc aac agc atc aac aac aac aac ggt agc caa ttc tat ctg	1116
Gly Gly Gly Asn Ser Ile Asn Asn Asn Asn Asn Gly Ser Gln Phe Tyr Leu	
260 265 270	
ccg cta agc cca ccg ctg agc atg agc aca gga tcg gac cgg gaa tcg	1164
Pro Leu Ser Pro Pro Leu Ser Met Ser Thr Gly Ser Asp Arg Glu Ser	
275 280 285	
ccc acc gga tca ctg tcc ctc agc ccc acc aac tcg ttg acc agc ttc	1212
Pro Thr Gly Ser Leu Ser Leu Ser Pro Thr Asn Ser Leu Thr Ser Phe	
290 295 300	

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ctg ggc atg agc atg ggc atc ggc cag ggc atg atc atc ggt cag ggt Leu Gly Met Ser Met Gly Ile Gly Gln Gly Met Ile Ile Gly Gln Gly 340 345 350	1356
ttg gga atg gga cat cat gga ccg gcc aca ccg ccg gag agc ccc aat Leu Gly Met Gly His His Gly Pro Ala Thr Pro Pro Glu Ser Pro Asn 355 360 365	1404
gtg ccc ata tcg cca gtg cat aca cca cca ccg tac gat gtg gtg gtc Val Pro Ile Ser Pro Val His Thr Pro Pro Pro Tyr Asp Val Val Val 370 375 380	1452
agt gga tct gga gcg ggc aac aat agc gtt ggc agc aag cag ctc ctg Ser Gly Ser Gly Ala Gly Asn Asn Ser Val Gly Ser Lys Gln Leu Leu 385 390 395 400	1500
cag aag agc gtc agc aca ccg atg cag cag gag gat acg ccc agg ttg Gln Lys Ser Val Ser Thr Pro Met Gln Gln Glu Asp Thr Pro Arg Leu 405 410 415	1548
ccg gtt ttc aac cgt ctc agc tcc ggt gtg gag gcc tac cag cag cag Pro Val Phe Asn Arg Leu Ser Ser Gly Val Glu Ala Tyr Gln Gln Gln 420 425 430	1596
tcc aat ttg gga ctc taa acgcgtggca gtctgcgaaa caaaattgaa Ser Asn Leu Gly Leu 435	1644
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cgcagtccaa tttgaaacgc aaatatgcca aggcaaatgg atttccggtg gcgtaacttc	1824
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gaccccttgat atcaattctc tcattgctgt gacagtcaaa cgtaatcggt atacaataat	1944
cggtatatga gaaggaccga attacggact actacgggac aattagttag atagatacgt	2004
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 <212> PRT
 <213> Drosophila melanogaster

<400> 17

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Leu Gly Asp Phe Asp Cys Asn Glu Val Arg Lys Glu Ile Arg Met Leu
35 40 45

Leu Ala His Gly Ala Asn Leu Asp Gln Gln His Gln Gln Gln Pro His
50 55 60

Arg His His Gly Gly Leu Thr Arg Thr Ile Ser Gln Pro Ala Gln Leu
65 70 75 80

Ile Gln Gln Gln Gln Gln Gln His Gln Gln Gln Gln Gln Gln Gln
85 90 95

Pro Pro Val Ala Ser Leu Val Thr Ile Thr Glu Asn Leu Gly Asn Met
100 105 110

Asn Leu His Arg Lys Leu Glu Arg Thr Gln Ser Glu Pro Leu Pro Pro
115 120 125

Gln Gln Pro Met Asn Thr Ser Arg Tyr Lys Thr Glu Leu Cys Arg Pro
130 135 140

Phe Glu Glu Ala Gly Glu Cys Lys Tyr Gly Glu Lys Cys Gln Phe Ala
145 150 155 160

His Gly Ser His Glu Leu Arg Asn Val His Arg His Pro Lys Tyr Lys
165 170 175

Thr Glu Tyr Cys Arg Thr Phe His Ser Val Gly Phe Cys Pro Tyr Gly
180 185 190

Pro Arg Cys His Phe Val His Asn Ala Asp Glu Ala Arg Ala Gln Gln
195 200 205

Ala Ala Gln Ala Ala Lys Ser Ser Thr Gln Ser Gln Ser Gln Ser Gln
210 215 220

Gln Ser Ser Ser Gln Asn Phe Ser Pro Lys Ser Asn Gln Ser Ser Asn
 225 230 235 240

Gln Ser Ser Asn Ser Ser Ser Ser Ser Ser Ser Gly Gly Gly Gly
 245 250 255

Gly Gly Gly Asn Ser Ile Asn Asn Asn Asn Gly Ser Gln Phe Tyr Leu
 260 265 270

Pro Leu Ser Pro Pro Leu Ser Met Ser Thr Gly Ser Asp Arg Glu Ser
 275 280 285

Pro Thr Gly Ser Leu Ser Leu Ser Pro Thr Asn Ser Leu Thr Ser Phe
 290 295 300

Pro Phe His Asp Ala Leu Gln His Gly Tyr Leu Ala Ser Asn Gly Ala
 305 310 315 320

Lys Ser Asn Ser Ser Ala Ser Ser Thr Ser Ser Ala Ser Gly Met Gly
 325 330 335

Leu Gly Met Ser Met Gly Ile Gly Gln Gly Met Ile Ile Gly Gln Gly
 340 345 350

Leu Gly Met Gly His His Gly Pro Ala Thr Pro Pro Glu Ser Pro Asn
 355 360 365

Val Pro Ile Ser Pro Val His Thr Pro Pro Pro Tyr Asp Val Val Val
 370 375 380

Ser Gly Ser Gly Ala Gly Asn Asn Ser Val Gly Ser Lys Gln Leu Leu
 385 390 395 400

Gln Lys Ser Val Ser Thr Pro Met Gln Gln Glu Asp Thr Pro Arg Leu
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Ser Asn Leu Gly Leu
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 Gly
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aac aag atg ctc aac tat agt gct ccc agt gca ggg ggt tgc ctg ctg 824
 Asn Lys Met Leu Asn Tyr Ser Ala Pro Ser Ala Gly Gly Cys Leu Leu
 5 10 15

gac aga aag gca gtg ggc acc cct gct ggt ggg ggc ttc cct cgg agg 872
 Asp Arg Lys Ala Val Gly Thr Pro Ala Gly Gly Gly Phe Pro Arg Arg
 20 25 30

cac tca gtc acc ctg ccc agc tcc aag ttc cac cag aac cag ctc ctc 920
 His Ser Val Thr Leu Pro Ser Ser Lys Phe His Gln Asn Gln Leu Leu
 35 40 45

agc agc ctc aag ggt gag cca gcc ccc gct ctg agc tcg cga gac agc 968
 Ser Ser Leu Lys Gly Glu Pro Ala Pro Ala Leu Ser Ser Arg Asp Ser
 50 55 60 65

cgc ttc cga gac cgc tcc ttc tcg gaa ggg ggc gag cgg ctg ctg ccc 1016
 Arg Phe Arg Asp Arg Ser Phe Ser Glu Gly Gly Glu Arg Leu Leu Pro

70					75					80						
acc	cag	aag	cag	ccc	ggg	ggc	ggc	cag	gtc	aac	tcc	agc	cgc	tac	aag	1064
Thr	Gln	Lys	Gln	Pro	Gly	Gly	Gly	Gln	Val	Asn	Ser	Ser	Arg	Tyr	Lys	
			85					90					95			
acg	gag	ctg	tgc	cgc	ccc	ttt	gag	gaa	aac	ggg	gcc	tgt	aag	tac	ggg	1112
Thr	Glu	Leu	Cys	Arg	Pro	Phe	Glu	Glu	Asn	Gly	Ala	Cys	Lys	Tyr	Gly	
		100					105					110				
gac	aag	tgc	cag	ttc	gca	cac	ggc	atc	cac	gag	ctc	cgc	agc	ctg	acc	1160
Asp	Lys	Cys	Gln	Phe	Ala	His	Gly	Ile	His	Glu	Leu	Arg	Ser	Leu	Thr	
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cgc	cac	ccc	aag	tac	aag	acg	gag	ctg	tgc	cgc	acc	ttc	cac	acc	atc	1208
Arg	His	Pro	Lys	Tyr	Lys	Thr	Glu	Leu	Cys	Arg	Thr	Phe	His	Thr	Ile	
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ggc	ttt	tgc	ccc	tac	ggg	ccc	cgc	tgc	cac	ttc	atc	cac	aac	gct	gaa	1256
Gly	Phe	Cys	Pro	Tyr	Gly	Pro	Arg	Cys	His	Phe	Ile	His	Asn	Ala	Glu	
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gag	cgc	cgt	gcc	ctg	gcc	ggg	gcc	cgg	gac	ctc	tcc	gct	gac	cgt	ccc	1304
Glu	Arg	Arg	Ala	Leu	Ala	Gly	Ala	Arg	Asp	Leu	Ser	Ala	Asp	Arg	Pro	
			165				170						175			
cgc	ctc	cag	cat	agc	ttt	agc	ttt	gct	ggg	ttt	ccc	agt	gcc	gct	gcc	1352
Arg	Leu	Gln	His	Ser	Phe	Ser	Phe	Ala	Gly	Phe	Pro	Ser	Ala	Ala	Ala	
		180					185					190				
acc	gcc	gct	gcc	acc	ggg	ctg	ctg	gac	agc	ccc	acg	tcc	atc	acc	cca	1400
Thr	Ala	Ala	Ala	Thr	Gly	Leu	Leu	Asp	Ser	Pro	Thr	Ser	Ile	Thr	Pro	
	195					200					205					
ccc	cct	att	ctg	agc	gcc	gat	gac	ctc	ctg	ggc	tca	cct	acc	ctg	ccc	1448
Pro	Pro	Ile	Leu	Ser	Ala	Asp	Asp	Leu	Leu	Gly	Ser	Pro	Thr	Leu	Pro	
210					215					220					225	
gat	ggc	acc	aat	aac	cct	ttt	gcc	ttc	tcc	agc	cag	gag	ctg	gca	agc	1496
Asp	Gly	Thr	Asn	Asn	Pro	Phe	Ala	Phe	Ser	Ser	Gln	Glu	Leu	Ala	Ser	
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ctc	ttt	gcc	cct	agc	atg	ggg	ctg	ccc	ggg	ggg	ggc	tcc	ccg	acc	acc	1544
Leu	Phe	Ala	Pro	Ser	Met	Gly	Leu	Pro	Gly	Gly	Gly	Ser	Pro	Thr	Thr	
			245				250						255			
ttc	ctc	ttc	cgg	ccc	atg	tcc	gag	tcc	cct	cac	atg	ttt	gac	tct	ccc	1592
Phe	Leu	Phe	Arg	Pro	Met	Ser	Glu	Ser	Pro	His	Met	Phe	Asp	Ser	Pro	
		260					265					270				
ccc	agc	cct	cag	gat	tct	ctc	tgc	gac	cag	gag	ggc	tac	ctg	agc	agc	1640
Pro	Ser	Pro	Gln	Asp	Ser	Leu	Ser	Asp	Gln	Glu	Gly	Tyr	Leu	Ser	Ser	
	275					280					285					
tcc	agc	agc	agc	cac	agt	ggc	tca	gac	tcc	ccg	acc	ttg	gac	aac	tca	1688
Ser	Ser	Ser	Ser	His	Ser	Gly	Ser	Asp	Ser	Pro	Thr	Leu	Asp	Asn	Ser	
290					295					300					305	

aga cgc ctg ccc atc ttc agc aga ctt tcc atc tca gat gac taa	1733
Arg Arg Leu Pro Ile Phe Ser Arg Leu Ser Ile Ser Asp Asp	
310 315	
gccagggtag ggagggacct cctgcctact ccagccccta ccctgcaccc acatcccata	1793
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 <212> PRT
 <213> Homo sapiens

<400> 19

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Arg His Ser Val Thr Leu Pro Ser Ser Lys Phe His Gln Asn Gln Leu
 35 40 45

Leu Ser Ser Leu Lys Gly Glu Pro Ala Pro Ala Leu Ser Ser Arg Asp
 50 55 60

Ser Arg Phe Arg Asp Arg Ser Phe Ser Glu Gly Gly Glu Arg Leu Leu
 65 70 75 80

Pro Thr Gln Lys Gln Pro Gly Gly Gly Gln Val Asn Ser Ser Arg Tyr
 85 90 95

Lys Thr Glu Leu Cys Arg Pro Phe Glu Glu Asn Gly Ala Cys Lys Tyr
 100 105 110

Gly Asp Lys Cys Gln Phe Ala His Gly Ile His Glu Leu Arg Ser Leu
 115 120 125

Thr Arg His Pro Lys Tyr Lys Thr Glu Leu Cys Arg Thr Phe His Thr
 130 135 140

Ile Gly Phe Cys Pro Tyr Gly Pro Arg Cys His Phe Ile His Asn Ala
 145 150 155 160

Glu Glu Arg Arg Ala Leu Ala Gly Ala Arg Asp Leu Ser Ala Asp Arg
 165 170 175

Pro Arg Leu Gln His Ser Phe Ser Phe Ala Gly Phe Pro Ser Ala Ala
 180 185 190

Ala Thr Ala Ala Ala Thr Gly Leu Leu Asp Ser Pro Thr Ser Ile Thr
 195 200 205

Pro Pro Pro Ile Leu Ser Ala Asp Asp Leu Leu Gly Ser Pro Thr Leu
 210 215 220

Pro Asp Gly Thr Asn Asn Pro Phe Ala Phe Ser Ser Gln Glu Leu Ala
 225 230 235 240

Ser Leu Phe Ala Pro Ser Met Gly Leu Pro Gly Gly Gly Ser Pro Thr
 245 250 255

Thr Phe Leu Phe Arg Pro Met Ser Glu Ser Pro His Met Phe Asp Ser
 260 265 270

Pro Pro Ser Pro Gln Asp Ser Leu Ser Asp Gln Glu Gly Tyr Leu Ser
 275 280 285

Ser Ser Ser Ser Ser His Ser Gly Ser Asp Ser Pro Thr Leu Asp Asn
 290 295 300

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 305 310 315

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 <212> DNA
 <213> *Saccharomyces cerevisiae*

<220>

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<222> (427)..(1404)

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ctcacgtctt tgatcagtgt gagcagttac taatatactg gatcagagaa cattaactca	240
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ctctcttaac aagtcacatc ttatttagcc ttttcaccca taagttgatt gtaaagccgt	360
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ctagcc atg atg ccg aat gtt gct cca aac agc tac tat tta aac ata	468
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ccg aat gcc aat tcg acc tca acg act acg tcc tcg atc ttt tct gat	516
Pro Asn Ala Asn Ser Thr Ser Thr Thr Ser Ser Ile Phe Ser Asp	
15 20 25 30	
ctc aac aag gag tac gag tca aag att aaa gaa atc gaa gaa tat tat	564
Leu Asn Lys Glu Tyr Glu Ser Lys Ile Lys Glu Ile Glu Glu Tyr Tyr	
35 40 45	
ata aag aca ctg ctc aat gaa aat acc gat aat gat gac agc agc agc	612
Ile Lys Thr Leu Leu Asn Glu Asn Thr Asp Asn Asp Asp Ser Ser Ser	
50 55 60	
tcc gag ggg cat aat ata aat gaa acg gac att tta agt gaa tac tca	660
Ser Glu Gly His Asn Ile Asn Glu Thr Asp Ile Leu Ser Glu Tyr Ser	
65 70 75	
cca agg cct tct cct tgg tta cca tcc aaa cca aac tgt tat cat ccg	708
Pro Arg Pro Ser Pro Trp Leu Pro Ser Lys Pro Asn Cys Tyr His Pro	
80 85 90	
ttg gga gat ttt aaa gac ttg atc ata tca gat tcc aga cct aca aat	756
Leu Gly Asp Phe Lys Asp Leu Ile Ile Ser Asp Ser Arg Pro Thr Asn	
95 100 105 110	
aca tta cct att aat aac cct ttc gca ggc aat aat aac atc tca aca	804
Thr Leu Pro Ile Asn Asn Pro Phe Ala Gly Asn Asn Asn Ile Ser Thr	
115 120 125	
ctt gct aca act gag aaa aaa cgt aag aaa agg tca ctc gaa gtt aga	852
Leu Ala Thr Thr Glu Lys Lys Arg Lys Lys Arg Ser Leu Glu Val Arg	
130 135 140	
gtt aac cct act tac acg aca agt gca ttt tca tta ccc ctg aca gcg	900

Val Asn Pro Thr Tyr Thr Thr Ser Ala Phe Ser Leu Pro Leu Thr Ala	
145 150 155	
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Glu Asn Leu Gln Lys Leu Ser Gln Val Asp Ser Gln Ser Thr Gly Leu	
160 165 170	
cca tac aca ctt cca att cag aaa aca aca aaa ctg gaa cct tgt aga	996
Pro Tyr Thr Leu Pro Ile Gln Lys Thr Thr Lys Leu Glu Pro Cys Arg	
175 180 185 190	
agg gca cct ttg cag ctt cct caa tta gtc aat aag acc tta tac aaa	1044
Arg Ala Pro Leu Gln Leu Pro Gln Leu Val Asn Lys Thr Leu Tyr Lys	
195 200 205	
act gag ctc tgt gaa tct ttt act att aaa ggc tat tgt aag tat gga	1092
Thr Glu Leu Cys Glu Ser Phe Thr Ile Lys Gly Tyr Cys Lys Tyr Gly	
210 215 220	
aat aaa tgc caa ttt gct cat ggt ctt aat gaa ctg aaa ttc aag aaa	1140
Asn Lys Cys Gln Phe Ala His Gly Leu Asn Glu Leu Lys Phe Lys Lys	
225 230 235	
aaa tca aac aat tat aga act aaa cct tgc ata aat tgg tcg aag tta	1188
Lys Ser Asn Asn Tyr Arg Thr Lys Pro Cys Ile Asn Trp Ser Lys Leu	
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ggc tac tgt ccg tac ggt aag cgt tgc tgt ttc aaa cac ggt gat gat	1236
Gly Tyr Cys Pro Tyr Gly Lys Arg Cys Cys Phe Lys His Gly Asp Asp	
255 260 265 270	
aag gac gtt gaa ata tat caa aat gct aac gat gga aga agt aag gat	1284
Lys Asp Val Glu Ile Tyr Gln Asn Ala Asn Asp Gly Arg Ser Lys Asp	
275 280 285	
acg gcg ttg act cca ctt cct act tcc cta gcc cca agc aac aac gat	1332
Thr Ala Leu Thr Pro Leu Pro Thr Ser Leu Ala Pro Ser Asn Asn Asp	
290 295 300	
aat atc act aat ttg agt aag cct agg aac tta cat act agt gtt aaa	1380
Asn Ile Thr Asn Leu Ser Lys Pro Arg Asn Leu His Thr Ser Val Lys	
305 310 315	
gca ttg caa agg atg act tgg tag tcggtcaaca acaaagccct ttgaatattt	1434
Ala Leu Gln Arg Met Thr Trp	
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<400> 21

Met Met Pro Asn Val Ala Pro Asn Ser Tyr Tyr Leu Asn Ile Pro Asn
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Ala Asn Ser Thr Ser Thr Thr Thr Ser Ser Ile Phe Ser Asp Leu Asn
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Lys Glu Tyr Glu Ser Lys Ile Lys Glu Ile Glu Glu Tyr Tyr Ile Lys
35 40 45

Thr Leu Leu Asn Glu Asn Thr Asp Asn Asp Asp Ser Ser Ser Ser Glu
50 55 60

Gly His Asn Ile Asn Glu Thr Asp Ile Leu Ser Glu Tyr Ser Pro Arg
65 70 75 80

Pro Ser Pro Trp Leu Pro Ser Lys Pro Asn Cys Tyr His Pro Leu Gly
85 90 95

Asp Phe Lys Asp Leu Ile Ile Ser Asp Ser Arg Pro Thr Asn Thr Leu
100 105 110

Pro Ile Asn Asn Pro Phe Ala Gly Asn Asn Asn Ile Ser Thr Leu Ala
115 120 125

Thr Thr Glu Lys Lys Arg Lys Lys Arg Ser Leu Glu Val Arg Val Asn
130 135 140

Pro Thr Tyr Thr Thr Ser Ala Phe Ser Leu Pro Leu Thr Ala Glu Asn
145 150 155 160

Leu Gln Lys Leu Ser Gln Val Asp Ser Gln Ser Thr Gly Leu Pro Tyr
165 170 175

Thr Leu Pro Ile Gln Lys Thr Thr Lys Leu Glu Pro Cys Arg Arg Ala
180 185 190

Pro Leu Gln Leu Pro Gln Leu Val Asn Lys Thr Leu Tyr Lys Thr Glu
195 200 205

Leu Cys Glu Ser Phe Thr Ile Lys Gly Tyr Cys Lys Tyr Gly Asn Lys
210 215 220

Cys Gln Phe Ala His Gly Leu Asn Glu Leu Lys Phe Lys Lys Lys Ser
225 230 235 240

Asn Asn Tyr Arg Thr Lys Pro Cys Ile Asn Trp Ser Lys Leu Gly Tyr
245 250 255

Cys Pro Tyr Gly Lys Arg Cys Cys Phe Lys His Gly Asp Asp Lys Asp
260 265 270

Val Glu Ile Tyr Gln Asn Ala Asn Asp Gly Arg Ser Lys Asp Thr Ala
275 280 285

Leu Thr Pro Leu Pro Thr Ser Leu Ala Pro Ser Asn Asn Asp Asn Ile
290 295 300

Thr Asn Leu Ser Lys Pro Arg Asn Leu His Thr Ser Val Lys Ala Leu
305 310 315 320

Gln Arg Met Thr Trp
325